REMARKS

This Office Action Response is submitted in response to the outstanding non-final Office Action, dated January 19, 2007. Claims 1-3, 17-19, 23-25 and 29 are presently pending in the above-identified patent application. Claims 1, 3, 17, 19 and 23 are herein proposed to be amended. Support for the amendments can be found, for example, on page 7, lines 12-17, page 6, lines 5-18, FIGS. 1 and 11-15, page 6, lines 21-25, page 12, lines 23-27, page 9, lines 16-19, page 20, lines 17-25 and page 23, lines 16-22.

In the outstanding Office Action, the Examiner rejected claims 1-3, 17-19, 23-25 and 29 under 35 U.S.C. §101 as allegedly being directed to non-statutory subject matter. Also, the Examiner rejected claims 1-3, 17-19, 23-25 and 29 under 35 U.S.C. §112, first paragraph, as allegedly failing to comply with the enablement requirement.

The comments of the Examiner in forming the objection and rejections are acknowledged and have been carefully considered.

FORMAL REJECTIONS

As mentioned above, the Examiner rejected claims 1-3, 17-19, 23-25 and 29 under 35 U.S.C. §101 as allegedly being directed to non-statutory subject matter. On page 3 of the Office Action, the Examiner states that

> [t]his rejection could be overcome by amending the claims to recite that a result of the method is "displayed" or "outputted" (e.g. output to a user, a display, a memory, or another computer, etc.). ...

Applicants respectfully assert the amendments to claims 1, 3, 17, 19 and 23 overcome the rejection. As currently amended, independent claims 1, 17 and 23 include the limitation of outputting a characterization of a gene expression of an unknown sample to at least one of a computer and a user. As stated on page 7, line 14, of the specification, the processor (as illustrated in FIG. 1) implements the methods, steps and functions disclosed in the specification. Additionally, FIG. 1 also illustrates that the processor can output data (e.g., gene characterization from an unknown sample) to a computer network that comprises one or more additional

computers. Furthermore, FIGS. 11-15 illustrate examples of characterization outputs, as generated by the claimed invention.

Consequently, Applicants respectfully assert that amended independent claims 1, 17 and 23, and the claims dependent therefrom, produce a real-world result, and therefore overcome the
5   rejection.

Also, the Examiner rejected claims 1-3, 17-19, 23-25 and 29 under 35 U.S.C §112, first paragraph, as allegedly failing to comply with the enablement requirement. On page 5 of the Office Action, the Examiner asserts that
10   [t]he specification fails to teach how to transformed gene expression

            signals to determine gene expression patterns. The instantly amended claims are

            further drawn to characterizing gene expression of an unknown sample by

            comparing gene expression of an unknown sample with gene expression patterns.

            The specification fails to teach how to correlate gene expression of an unknown
15   sample with gene expression patterns.

With respect to the statement by the Examiner: "[t]he specification fails to teach how to use transformed gene expression signals to determine gene expression patterns," Applicants respectfully point to, as an example, page 15, lines 2-9, of the specification:
20   Of all the possible patterns in a phenotype matrix, some of the patterns
            will be maximal. These maximal patterns are submatrices of the phenotype
            matrix. In step 250, these maximal patterns are determined. There are a variety of
            well known pattern-finding algorithms and techniques that may be used in this
            step.
25   For instance, the SPLASH algorithm may be used. Full details of the
            SPLASH algorithm are given in Califano, A., "SPLASH: Structural Pattern
            Localization Algorithm by Sequential Histograming," Bioinformatics 16, 341-
            357, 2000, the disclosure of which is incorporated by reference herein.

30   Also, with respect to the statement by the Examiner: "[t]he instantly amended claims are further drawn to characterizing gene expression of an unknown sample by comparing gene

expression of an unknown sample with gene expression patterns. The specification fails to teach how to correlate gene expression of an unknown sample with gene expression patterns," Applicants respectfully point to, as an example, the specification beginning on page 19, line 14, of the specification:

5   To determine if a new microarray sample fits the phenotype model of a jk-pattern Π_l for the expression values $(v_1, v_2, ..., v_k)$ over the k genes that constitute Π_l, it is scored by the logarithm of the ratio of the two probability densities, as described in Welch, B.L., "Note on Discriminant Functions," Biometrika, Vol 31, pp. 218-220, 1939, the disclosure of which is incorporated
10   herein by reference:

$$S_l = \log\left[\frac{P^+(v_1,...,v_k)}{P^-(v_1,...,v_k)}\right] \approx \sum_{i=1}^{k} \log[P_i^+(v_i)] - \sum_{i=1}^{k} \log[P_i^-(v_i)] \tag{7}$$

          Using this score, it can easily be determined whether promiscuous patterns
15   are contained in the set of statistically significant patterns. Patterns with positive values of S_l for samples taken from the control set are considered promiscuous. Next, the statistically significant patterns are preferably assigned a promiscuity index:

$$\wp_l = \sum_{S_l(v)>0} S_l(\mathbf{v} \in ControlSet) \tag{8}$$

20   where the sum runs over all the samples in the control set for which $S_l > 0$. Patterns whose $S_l < 0$ for all samples in the control set have a promiscuity index of zero. Patterns can now be sorted according to the promiscuity index, with the
25   least promiscuous pattern first.

Furthermore, Applicants respectfully assert that the amendments to claims 1, 3, 17, 19 and 23 overcome the rejection. Applicants submit that the specification sufficiently enables the claim limitations of the amended claims. As means of example, the amendments to independent
30 claims 1, 17 and 23 include the following limitations.

One limitation reads "determining a plurality of gene expression signals for a gene, wherein said plurality of gene expression signals comprise control data and phenotype data." On page 6, lines 21-25 of the specification, it describes "an initial set of expression data for one

phenotype (generally called the control set and containing information from healthy cells)" and "a set of expression data from another phenotype (generally called the phenotype set and containing information from unhealthy cells)." Also, on page 12, lines 23-27 of the specification, it describes that "expression levels are determined by examining the fluorescence

5   of locations on a microarray." Applicants respectfully submit that the above-referenced limitation is sufficiently enabled by the specification.

Another limitation reads "transforming said plurality of gene expression signals, wherein said transforming results in transformed gene expression signals having a uniform distribution of said gene expression signals within a selected interval in said control data." On page 14, lines 9-

10 17 of the specification, it describes that "transformations are derived" and that "during this process, the actual probability density distribution may be integrated, or a function derived that estimates the actual probability density distribution and that is then integrated." Applicants respectfully submit that the above-referenced limitation is sufficiently enabled by the specification.

15 Another limitation reads "using said transformed gene expression signals to determine one or more gene expression patterns by searching said transformed gene expression signals for said one or more gene expression patterns, wherein the one or more gene expression patterns characterize said control data and said phenotype data." On page 9, lines 16-19 of the specification, it describes that one or more embodiments of the present invention "will search the

20 transformed phenotype matrix 145 for patterns." Applicants respectfully submit that the above-referenced limitation is sufficiently enabled by the specification.

Yet another limitation reads "characterizing gene expression of an unknown sample by determining one or more gene expression patterns for said unknown sample and comparing said one or more gene expression patterns of said unknown sample with said one or more gene

25 expression patterns that characterize said control data and said phenotype data to characterize said unknown sample as either said control data or said phenotype data." On page 20, lines 17-

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25 of the specification, it is stated that "[e]ach sample is a vector of expressions, where each expression corresponds to one gene of the phenotype matrix," and that one or more embodiments of the invention "classify a sample as either in the phenotype set or in the control set or in neither." Applicants respectfully submit that the above-referenced limitation is sufficiently enabled by the specification.

Also, a limitation reads as "outputting said characterization to at least one of a computer and a user." As described above, support for this amended limitation can be found, for example, at page 7, lines 12-17, page 6, lines 5-18, and FIGS. 1 and 11-15 of the specification.

Given the above remarks, Applicants respectfully request reconsideration and withdrawal of the rejections of claims 1-3, 17-19, 23-25 and 29 under 35 U.S.C. §112, first paragraph.

In view of the foregoing, Applicants submit that all of the pending claims, i.e., claims 1-3, 17-19, 23-25 and 29, are in condition for allowance and such favorable action is earnestly solicited.

If any outstanding issues remain, or if the Examiner has any further suggestions for expediting allowance of this application, the Examiner is invited to contact the undersigned at the telephone number indicated below.

The Examiner's attention to this matter is appreciated.

Respectfully submitted,

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